

9598-066

(SHEET 1 OF 16)

ACGTTGACAC AGGAATGAAG AGTGTATTGG CTGAATCTTC AAGCAGAGGC GATATTGACC ATGTGCTTT TAAATTGGCC TCGGTGACCC GCCCCACTTGG TGTAAGGAA GAACCGGCCA AAGGGAGGGC CTGAAGGACC TCCACAGGAG TGTGAGCAGC ACTGCTTCAG CAACAAAGCC TCAGGTCCAC ATCTTGGAA GAAT ATG GCC ACT TCC TGG GGG GCT GTC TTC Met Ala Thr Ser Trp Gly Ala Val Phe 1 5	60 120 180 231
ATG CTG ATC ATA GCC TGC GTT GGC AGC ACT GTC TTC TAC AGA GAA CAG Met Leu Ile Ile Ala Cys Val Gly Ser Thr Val Phe Tyr Arg Glu Gln 10 15 20 25	279
CAG ACC TGG TTT GAA GGT GTC TTC TTG TCT TCC ATG TGC CCC ATT AAT Gln Thr Trp Phe Glu Gly Val Phe Leu Ser Ser Met Cys Pro Ile Asn 30 35 40	327
GTC AGT GCC GGC ACC TTT TAT GGA ATT ATG TTT GAT GCG GGC AGC ACT Val Ser Ala Gly Thr Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr 45 50 55	375
GGA ACT CGG ATT CAT GTT TAC ACT TTT GTG CAG AAA ACA GCA GGA CAG Gly Thr Arg Ile His Val Tyr Thr Phe Val Gln Lys Thr Ala Gly Gln 60 65 70	423
CTC CCC TTT CTG GAA GGT GAA ATT TTT GAT TCT GTG AAG CCG GGA CTT Leu Pro Phe Leu Glu Gly Glu Ile Phe Asp Ser Val Lys Pro Gly Leu 75 80 85	471
TCT GCT TTT GTG GAT CAG CCC AAA CAG GGT GCT GAG ACT GTC CAG GAG Ser Ala Phe Val Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Glu 90 95 100 105	519
CTC TTG GAG GTG GCC AAA GAC TCG ATC CCC AGA AGC CAC TGG GAA AGG Leu Leu Glu Val Ala Lys Asp Ser Ile Pro Arg Ser His Trp Glu Arg 110 115 120	567
ACC CCG GTG GTT CTG AAA GCA ACG GCC GGA CTC CGT TTG CTG CCT GAG Thr Pro Val Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Pro Glu 125 130 135	615
CAG AAA GCC CAG GCT CTG CTC TTG GAG GTA GAG GAG ATC TTC AAG AAT Gln Lys Ala Gln Ala Leu Leu Leu Glu Val Glu Glu Ile Phe Lys Asn 140 145 150	663
TCA CCT TTC CTG GTC CCA GAT GGC AGC GTT AGC ATC ATG GAT GGG TCC Ser Pro Phe Leu Val Pro Asp Gly Ser Val Ser Ile Met Asp Gly Ser 155 160 165	711
TAT GAA GGC ATA CTA GCC TGG GTT ACC GTG AAC TTT CTA ACA GGT CAG Tyr Glu Gly Ile Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln 170 175 180 185	759
CTG CAT GGT CGT GGC CAG GAG ACT GTG GGG ACC CTT GAC CTG GGG GGT Leu His Gly Arg Gly Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly 190 195 200	807
GCC TCC ACC CAA ATC ACG TTT CTA CCC CAG TTT GAG AAA ACC CTG GAA Ala Ser Thr Gln Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu 205 210 215	855
CAA ACA CCT AGG GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT Gln Thr Pro Arg Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr 220 225 230	903

FIG. 1

9598-066

(SHEET 2 OF 16)

TTT AAG CTC TAT ACA CAT AGT TAC TTG GGA TTT GGA CTG AAA GCT GCA Phe Lys Leu Tyr Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala 235 240 245	951
AGA CTG GCA ACT CTG GGA GCC CTG GAA GCA AAA GGG ACT GAT GGA CAT Arg Leu Ala Thr Leu Gly Ala Leu Glu Ala Lys Gly Thr Asp Gly His 250 255 260 265	999
ACG TTT CGA AGT GCC TGT TTA CCA AGA TGG TTG GAA GCA GAG TGG ATC Thr Phe Arg Ser Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile 270 275 280	1047
TTT GGG GGT GTG AAA TAC CAG TAT GGT GGT AAC CAA GAA GGG GAG ATG Phe Gly Val Lys Tyr Gln Tyr Gly Asn Gln Glu Gly Glu Met 285 290 295	1095
GGC TTT GAA CCC TGC TAT GCG GAA GTG CTG AGG GTA GTA CAG GGG AAA Gly Phe Glu Pro Cys Tyr Ala Glu Val Leu Arg Val Val Gln Gly Lys 300 305 310	1143
CTT CAC CAG CCA GAA GAA GTC CGA GGA AGC GCC TTC TAC GCT TTC TCT Leu His Gln Pro Glu Glu Val Arg Gly Ser Ala Phe Tyr Ala Phe Ser 315 320 325	1191
TAC TAC TAC GAT CGA GCC GCT GAC ACA CAC TTG ATC GAT TAT GAA AAG Tyr Tyr Tyr Asp Arg Ala Ala Asp Thr His Leu Ile Asp Tyr Glu Lys 330 335 340 345	1239
GGC GGG GTT TTA AAA GTT GAA GAT TTT GAA AGA AAA GCC AGA GAA GTG Gly Gly Val Leu Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val 350 355 360	1287
TGT GAC AAC TTG GGG AGC TTC TCC TCG GGC AGT CCT TTC CTC TGC ATG Cys Asp Asn Leu Gly Ser Phe Ser Ser Gly Ser Pro Phe Leu Cys Met 365 370 375	1335
GAC CTC ACT TAC ATC ACA GCC CTG TTG AAA GAT GGT TTG GGC TTT GCC Asp Leu Thr Tyr Ile Thr Ala Leu Leu Lys Asp Gly Leu Gly Phe Ala 380 385 390	1383
GAA CGG CAC CCT CTT ACA GCT CAC AAA GAA AGT GAA CAA CAT AGA GAC Glu Arg His Pro Leu Thr Ala His Lys Glu Ser Glu Gln His Arg Asp 395 400 405	1431
TGG TTG GGC CTT GGG GGC CAC CTT TCA CCT GCT CCA GTC TCT GGG CAT Trp Leu Gly Leu Gly His Leu Ser Pro Ala Pro Val Ser Gly His 410 415 420 425	1479
CAC CAG CTG AGG CCA AGC TCC ACC TCT GAA GCC TGC ATT TCT GAA CCA His Gln Leu Arg Pro Ser Ser Thr Ser Glu Ala Cys Ile Ser Glu Pro 430 435 440	1527
GTT TTC TCA CAG GAA GGC GTG GAC TCA GAG ACA TTT TCT GAC CTC TCT Val Phe Ser Gln Glu Gly Val Asp Ser Glu Thr Phe Ser Asp Leu Ser 445 450 455	1575
GGA AAA GCC TGG CCC GAA ACC CGT TAACTGGTTT TATAAGGAGG GAGGGTTTT Gly Lys Ala Trp Pro Glu Thr Arg 460 465	1629

Fig. 1 (cont'd.)

9598-066

(SHEET 3 OF 16)

TAGATGAGTC	TTGGCTCTTGA	GCCTAGTGAT	TTGGGCTTCA	ATGATTGCA	CATCTAATGT	1689
GAATAGCTCC	TAACCACTTG	GTGGGTGCAT	GGCTGGCACC	AGACTGTAAA	TCTTTGGGA	1749
TTCTTTGTAC	AGAGTCCTGC	AAAGGAAAAAA	AGAGAAAAGG	TTTGGAACTC	CATGCTAGAT	1809
TGCCGAGTTCA	GAGACAGGTC	CCTGGGGACC	AAAGAACAAAT	CTCGTTCAA	CCCTTGGATG	1869
CCTCATTGCT	TTGAATGGAT	TCATTTTGCG	TTATAAGCTG	ATTTACTGAA	ATCCCATAAC	1929
CCATCAATGC	TGTTAATTTC	TTTCTTCCTA	CCCTTATTAC	ATTCCCTACC	CTAAAAGCCT	1989
GGGGAAATA	CCTGGTTTG	CTTCCCCATCT	ATAATTGAGA	AAGAGGGGGG	AAAAGATACT	2049
GTATTAGAAT	TTGTGTGATC	CTGTGGCACA	ATAGATCAAC	CAACCCATT	AAAGCTTAAA	2109
AAAAAAAAAA						2119

FIG. 1 (cont'd.)

9598-066

HEET 4 OF (6)

peaNTPase	1	----MELGHNLTFLGFSPWPKITSSEYLGNNKLTTSRKTFPKGEPEISSYANVFDAGSTGSR
potapyrase	1	MLNQNSHFPFIHNMPLVLPSSLQKVNNAQTPRREHLSENSE..RVAWIFDAGSTGSR
mNTPase	1	WATSWGAIVPMHLIACVQSTVYREQOTMVEGYFHSNCPANVSAGAFYQGMFDAGSTGAR
yGDPase	1	KTPAIVIATIPYNDPGQLQDDEKTCQYPELADAKSQTSGTCSEHHAYVIMIDAGSTGSR
peaNTPase	57	IHVYVLFNQHMDPLHICKOVEYHKTTPGLSSVAMPCQAASLIPPLEQAEVVPPDPLQP
potapyrase	59	VHVAASDPAVLLPICHNNYEFMTEPGLSISYEDPRAAANSLPILLQAEGVVFQNLQS
mNTPase	61	IHVYVLFVQNTAGOLPPDEGGIFPDXKPGISAVHQPKQAAEYQBLLEVAKDCTPRSHWE
yGDPase	61	VHVAASDPAVLLPICHNNYEFMTEPGLSISYEDPRAAANSLPILLQAEGVVFQNLQS
peaNTPase	117	ATPVRLGATAGLRLLNCDASEKILSVRDLKLSNRSTF.NVCPDRVSIMDGTOEGSYLWVT
potapyrase	119	ATPVRLGATAGLRLLNCDASEKILSVRDLKLSNRSTF.HSDOMVTLGDCTOEGSYLMWAK
mNTPase	121	ATPVVLKATAGLRLLPQKACALDLEVEREFKN.SPF.DVFDGEVSIMDGSYWEGILAWVT
yGDPase	119	ATPVVLKATAGLRLLPQKACALDLEVEREFKN.SPF.DVFDGEVSIMDGSYWEGILAWVT
peaNTPase	176	VNVIALGNLGKAKTK..TVGVIDLGGGSVOMAYAVSKTTAKNAPKADGDPYKKVYLKG
potapyrase	178	INYILGNGLKDJKS..TTATIDLGGGSVOMAYAVSKTTAKNAPKADGDPYKKVYLKG
mNTPase	179	VNPDTGQDHGEQEE..TVGVIDLGGASTQITTELPOBK...TLEOTPRGILTSPEMPN
yGDPase	179	TNYILGNGCAGOPKLMIAVFDLGGGSVOMAYAV..TSPINEKIVDGHMKI..DNGFGD
peaNTPase	234	IPHELYVHSYLLFGGRASRAEILKL..
potapyrase	235	KDMLYVHSYLNIGQZAGRAEIPKA..
mNTPase	235	STEMLYTHSYLGFGLKAAALDTEGA..
yGDPase	234	ENMLYOFSHSYLGFGLKAAALDTEGA..
peaNTPase	276	TVGCEEPKATVYTSGA..NVAACNTIPEALKIENYCGPYHCTEGGLWNNGGGN..
potapyrase	277	SNVGDYDMVKPDKKES..SNKRCRSLTALHNGNQHMMHCTPNQVNGGGD..
mNTPase	279	ACLPRMLEAEWLPGCV..KXYYCCGQEOBHGTFPCYAZMLAVVQOKBHPPEZR..
yGDPase	294	EKYTLGSKETTYTIDFIGDPEPSAQCRPLPQDIEKQKQDQGQSPFCSENGVRQPSLVRTFK
peaNTPase	328	GOKNQVASSFSYLPDPTCHVDSIENPMLPDIETKAKEACALNFDAKSITPFLDKK
potapyrase	329	CORNIAASSPCEYICNOVHVDKAFPSGAHOBQDQYLNAAKVACQDNVADIKSIPKTKQK
mNTPase	322	GEA.FYAFSYWHDRAADTRHIDIE.KOGVHVEEDPERKAREVB..NLGSFESGSG..
yGDPase	354	ZENDIIFPSYTYDRAARPLGPFLPQDNEINDLAHVCKEETAVKVEEGHAGS..LDRL
peaNTPase	388	NWASYWCMDDLYQVLLVDFGIDPLQKITSQKELEYQDAAVPAAWPLGNAVEKAISALPK
potapyrase	389	NN..PYLCMDLTYIPLVLLVDFGIDPLQKITSQKELEYQDAAVPAAWPLGNAVEKAISALPK
mNTPase	374	...ECLCMDLTYITALLRDGLCPAERBLPAHKESEQHRDWLGLGGHILSPAPVSGHHQLR
yGDPase	411	ESDISHYCLDLISTOVSLLETGQDPLQREHRTGKMANKE..ICWCEGASUPFLKADNW
peaNTPase	448	FEREMYFV-----
potapyrase	448	HRRVABE-----
mNTPase	430	PSSTEGACISEPVTQSQEGVDSETPSDSLSCRAWPITR*
yGDPase	467	KCKHQSA-----

FIG. 2

9598-066

(SHEET 5 OF 16)

ACR I

	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
CD39	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
ratCD39	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
CD39L1	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
chickATPase	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
peantPase	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
potKOP1	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90</td										

9598-066

(SHEET 6 OF 16)

GTGGGGTCGT ATCCCGCGGG TGGAGGCCGG GGTGGCGCCG GCCGGGGCGG GGGAGCCCAA	60
AAGACCGGCT GCGCCTGCT CCCCGAAAAA GGGCACTCGT CTCCGTGGGT GTGGCGGAGC	120
GCGCGGTGCA TGAATGGGC TATGTGAATG AAAAAAGGTA TCCGTTATGA AACTTCCAGA	180
AAAACGAGCT ACATTTTCA GCAGCCGCAG CACGGTCCTT GGCAAACAAG G ATG AGA	237
Met Arg 1	
AAA ATA TCC AAC CAC GGG AGC CTG CGG GTG GCG AAG GTG GCA TAC CCC	285
Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro	
5 10 15	
CTG GGG CTG TGT GTG GGC GTG TTC ATC TAT GTT GCC TAC ATC AAG TGG	333
Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp	
20 25 30	
CAC CGG GCC ACC GCC ACC CAG GCC TTC TTC AGC ATC ACC AGG GCA GCC	381
His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala	
35 40 45 50	
CCG GGG GCC CGG TGG GGT CAG CAG GCC CAC AGC CCC CTG GGG ACA GCT	429
Pro Gly Ala Arg Trp Gly Gln Ala His Ser Pro Leu Gly Thr Ala	
55 60 65	
GCA GAC GGG CAC GAG GTC TTC TAC GGG ATC ATG TTT GAT GCA GGA AGC	477
Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser	
70 75 80	
ACT GGC ACC CGA GTA CAC GTC TTC CAG TTC ACC CGG CCC CCC AGA GAA	525
Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu	
85 90 95	
ACT CCC ACG TTA ACC CAC GAA ACC TTC AAA GCA GTG AAG CCA GGT CTT	573
Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu	
100 105 110	
TCT GCC TAT GCT GAT GTT GAA AAG AGC GCT CAG GGA ATC CGG GAA	621
Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu	
115 120 125 130	
CTA CTG GAT GTT GCT AAA CAG GAC ATT CCG TTC GAC TTC TGG AAG GCC	669
Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala	
135 140 145	
ACC CCT CTG GTC CTC AAG GCC ACA GCT GGC TTA CGC CTG TTA CCT GGA	717
Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly	
150 155 160	
GAA AAG GCC CAG AAG TTA CTG CAG AAG GTG AAA GAA GTA TTT AAA GCA	765
Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala	
165 170 175	
TCG CCT TTC CTT GTA GGG GAT GAC TGT GTT TCC ATC ATG AAC GGA ACA	813
Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr	
180 185 190	
GAT GAA GGC GTT TCG GCG TGG ATC ACC ATC AAC TTC CTG ACA GGC AGC	861
Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser	
195 200 205 210	
TTG AAA ACT CCA GGA GGG AGC AGC GTG GGC ATG CTG GAC TTG GGC GGA	909
Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly	
215 220 225	

FIG. 4

9598-066

(SHEET 7 OF 16)

GGA TCC ACT CAG ATC GCC TTC CTG CCA CGC GTG GAG GGC ACC CTG CAG Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln 230 235 240	957
GCC TCC CCA CCC GGC TAC CTG ACG GCA CTG CGG ATG TTT AAC AGG ACC Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr 245 250 255	1005
TAC AAG CTC TAT TCC TAC AGC TAC CTC GGG CTC GGG CTG ATG TCG GCA Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala 260 265 270	1053
CGC CTG GCG ATC CTG GGC GGC GTG GAG GGG CAG CCT GCT AAG GAT GGA Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly 275 280 285 290	1101
AAG GAG TTG GTC AGC CCT TGC TTG TCT CCC AGT TTC AAA GGA GAG TGG Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp 295 300 305	1149
GAA CAC GCA GAA GTC ACG TAC AGG GTT TCA GGG CAG AAA GCA GCG GCA Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala 310 315 320	1197
AGC CTG CAC GAG CTG TGT GCT GCC AGA GTG TCA GAG GTC CTT CAA AAC Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn 325 330 335	1245
AGA GTG CAC AGG ACG GAG GAA GTG AAG CAT GTG GAC TTC TAT GCT TTC Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe 340 345 350	1293
TCC TAC TAT TAC GAC CTT GCA GCT GGT GTG GGC CTC ATA GAT GCG GAG Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu 355 360 365 370	1341
AAG GGA GGC AGC CTG GTG GTG GGG GAC TTC GAG ATC GCA GCC AAG TAC Lys Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr 375 380 385	1389
GTG TGT CGG ACC CTG GAG ACA CAG CCG CAG AGC AGC CCC TTC TCA TGC Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys 390 395 400	1437
ATG GAC CTC ACC TAC GTC AGC CTG CTA CTC CAG GAG TTC GGC TTT CCC Met Asp Leu Thr Tyr Val Ser Leu Leu Gln Glu Phe Gly Phe Pro 405 410 415	1485
AGG AGC AAA GTG CTG AAG CTC ACT CGG AAA ATT GAC AAT GTT GAG ACC Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr 420 425 430	1533
AGC TGG GCT CTG GGG GCC ATT TTT CAT TAC ATC GAC TCC CTG AAC AGA Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg 435 440 445 450	1581
CAG AAG AGT CCA GCC TCA TAGTGGCCGA GCCATCCCTG TCCCCGTCAG CAGTGTCT Gln Lys Ser Pro Ala Ser 455	1637
GTGTGTCTGC ATAAACCCCTC CTGTCCTGGA CGTGACTTCA TCCCTGAGGGAG CCACAGCACA GGCCGTGCTG GCACCTTCTG CACACTGGCT CTGGGACTTG CAGAAGGCCT GGTGCTGCC TGGCATCAGC CTCTTCCAGT CACATCTGGC CAGAGGGCTG TCTGGACCTG GGCCCTGCTC 1697 1757 1817	

FIG. 4 (cont'd.)

9598-066

(MEET 8 OF 16)

AATGCCACCT	GTCTGCCTGG	GCTCCAAGTG	GGCAGGGACCA	GGACAGAAACC	ACAGGCACAC	1877
ACTGAGGGGG	CAGTGTGGCT	CCCTGCCTGT	CCCATCCCCA	TGCCCCGTCC	GCGGGGCTGT	1937
GGCTGCTGCT	GTGCATGTCC	CTGCGATGGG	AGTCTTGTCT	CCCAGCCTGT	CAGTTTCCTC	1997
CCCAGGGCAG	AGCTCCCCCTT	CCTGCAAGAG	TCTGGGAGGC	GGTGCAGGCT	GTCCCTGGCTG	2057
CTCTGGGGAA	GCCGAGGGAC	AGCCATAACA	CCCCCGGGAC	AGTAGGTCTG	GGCGGCACCA	2117
CTGGGAACTC	TGGACTTGAG	TGTGTTGCT	CTTCCTTGGG	TATGAATGTG	TGAGTTAACCC	2177
CAGAGGGCTG	CTCTCCTCAC	ACATTGTGTG	GTTGGGGTT	AATGATGGAG	GGAGACACCT	2237
CTTCATAGAC	GGCAGGTGCC	CACCTTCAG	GGAGTCTCCC	AGCATGGGCG	GATGCCGGC	2297
ATGAGCTGCT	GTAAACTATT	TGTGGCTGTG	CTGCTTGAGT	GACGTCTCTG	TCGTGTGGGT	2357
GCCAAGTGCT	TGTGTAGAAA	CTGTGTTCTG	AGCCCCCTTT	TCTGGACACC	AACTGTGTCC	2417
TGTGAATGTA	TCGCTACTGT	GAGCTGTTCC	CGCCTAGCCA	GGGCCATGTC	TTAGGTGCAG	2477
CTGTGCCACG	GGTCAGCTGA	GCCACAGTCC	CAGAACCAAG	CTCTCGGTGT	CTCGGGCAC	2537
CATCCGCCCA	CCTCGGGCTG	ACCCCCACCTC	CTCCATGGAC	AGTGTGAGCC	CCGGGCCGTG	2597
CATCCTGCTC	AGTGTGGCGT	CAGTGTGGG	GCTGAGCCCC	TTGAGCTGCT	TCAGTGAATG	2657
TACAGTGCCC	GGCACGAGCT	GAACCTCATG	TGTTCCACTC	CCAATAAAAG	GTTGACAGGG	2717
GCTTCTCCTT	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	AAAAAA		2762

Fig. 4 (cont'd)

9598-066

(SHEET 9 OF 16)

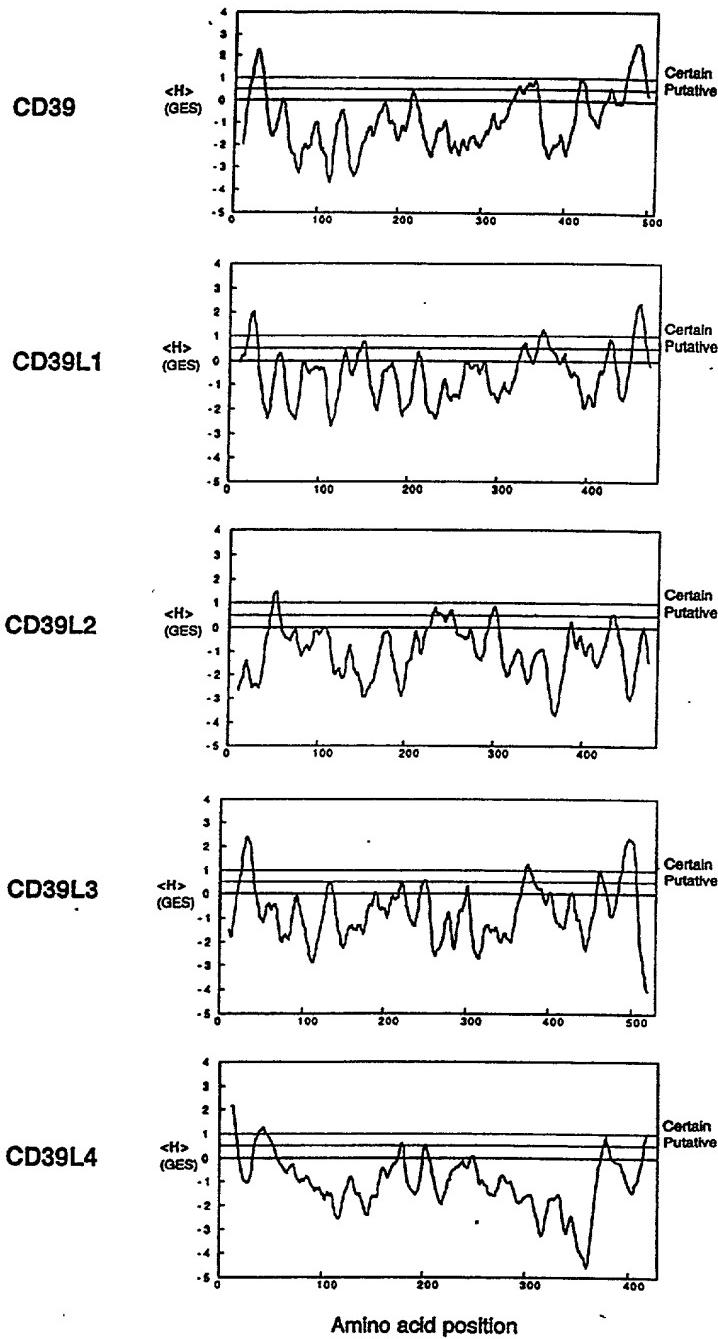


FIG. 5

9598-066

(SHEET 10 OF 16)

ACCCACGGCGT CTGGCCGCGG GCCGCCTCTG CGGCAGCGCT AGTCGCCTTC TCCGAATCGG CTCCGCACAG CTAGGAGAAA AG ATG TTC ACT GTG CTG ACC CGC CAA CCA TGT Met Phe Thr Val Leu Thr Arg Gln Pro Cys	60 112
1 5 10	
GAG CAA GCA GGC CTC AAG GCC CTC TAC CGA ACT CCA ACC ATC ATT GCC Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala	160
15 20 25	
TTG GTG GTC TTG CTT GTG AGT ATT GTG GTA CTT GTG AGT ATC ACT GTC Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val	208
30 35 40	
ATC CAG ATC CAC AAG CAA GAG GTC CTC CCT CCA GGA CTG AAG TAT GGT Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly	256
45 50 55	
ATT GTG CTG GAT GCC GGG TCT TCA AGA ACC ACA GTC TAC GTG TAT CAA Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln	304
60 65 70	
TGG CCA GCA GAA AAA GAG AAT AAT ACC GGA GTG GTC AGT CAA ACC TTC Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe	352
75 80 85 90	
AAA TGT AGT GTG AAA GGC TCT GGA ATC TCC AGC TAT GGA AAT AAC CCC Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro	400
95 100 105	
CAA GAT GTC CCC AGA GCC TTT GAG GAG TGT ATG CAA AAA GTC AAG GGG Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly	448
110 115 120	
CAG GTT CCA TCC CAC CTC CAC GGA TCC ACC CCC ATT CAC CTG GGA GCC Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala	496
125 130 135	
ACG GCT GGG ATG CGC TTG CTG AGG TTG CAA AAT GAA ACA GCA GCT AAT Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn	544
140 145 150	
GAA GTC CTT GAA AGC ATC CAA AGC TAC TTC AAG TCC CAG CCC TTT GAC Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp	592
155 160 165 170 175 180 185	
TTT AGG GGT GCT CAA ATC ATT TCT GGG CAA GAA GAA GGG GTA TAT GGA Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly	640
190 195 200	
TGG ATT ACA GCC AAC TAT TTA ATG GGA AAT TTC CTG GAG AAG AAC CTG Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu	688
205 210 215	
TGG CAC ATG TGG GTG CAC CCG CAT GGA GTG GAA ACC ACG GGT GCC CTG Trp His Met Trp Val His Pro His Gly Val Glu Thr Thr Gly Ala Leu	736
220 225 230	
GAC TTA GGT GGT GCC TCC ACC CAA ATA TCC TTC GTG GCA GGA GAG AAG Asp Leu Gly Gly Ala Ser Thr Gln Ile Ser Phe Val Ala Gly Glu Lys	784

FIG. 6

9598-066

SHEET II OF 16)

ATG GAT CTG AAC ACC AGC GAC ATC ATG CAG GTG TCC CTG TAT GGC TAC Met Asp Leu Asn Thr Ser Asp Ile Met Gln Val Ser Leu Tyr Gly Tyr 235 240 245 250	832
GTA TAC ACG CTC TAC ACA CAC AGC TTC CAG TGC TAT GGC CGG AAT GAG Val Tyr Thr Leu Tyr Thr His Ser Phe Gln Cys Tyr Gly Arg Asn Glu 255 260 265	880
GCT GAG AAG AAG TTT CTG GCA ATG CTC CTG CAG AAT TCT CCT ACC AAA Ala Glu Lys Lys Phe Leu Ala Met Leu Leu Gln Asn Ser Pro Thr Lys 270 275 280	928
AAC CAT CTC ACC AAT CCC TGT TAC CCT CGG GAT TAT AGC ATC AGC TTC Asn His Leu Thr Asn Pro Cys Tyr Pro Arg Asp Tyr Ser Ile Ser Phe 285 290 295	976
ACC ATG GGC CAT GTA TTT GAT AGC CTG TGC ACT GTG GAC CAG AGG CCA Thr Met Gly His Val Phe Asp Ser Leu Cys Thr Val Asp Gln Arg Pro 300 305 310	1024
GAA AGT TAT AAC CCC AAT GAT GTC ATC ACT TTT GAA GGA ACT GGG GAC Glu Ser Tyr Asn Pro Asn Asp Val Ile Thr Phe Glu Gly Thr Gly Asp 315 320 325 330	1072
CCA TCT CTG TGT AAG GAG AAG GTG GCT TCC ATA TTT GAC TTC AAA GCT Pro Ser Leu Cys Lys Glu Lys Val Ala Ser Ile Phe Asp Phe Lys Ala 335 340 345	1120
TGC CAT GAT CAA GAA ACC TGT TCT TTT GAT GGG GTT TAT CAG CCA AAG Cys His Asp Gln Glu Thr Cys Ser Phe Asp Gly Val Tyr Gln Pro Lys 350 355 360	1168
ATT AAA GGG CCA TTT GTG GCT TTT GCA GGA TTC TAC TAC ACA GCC AGT Ile Lys Gly Pro Phe Val Ala Phe Ala Gly Phe Tyr Tyr Thr Ala Ser 365 370 375	1216
GCT TTA AAT CTT TCA GGT AGC TTT TCC CTG GAC ACC TTC AAC TCC AGC Ala Leu Asn Leu Ser Gly Ser Phe Ser Leu Asp Thr Phe Asn Ser Ser 380 385 390	1264
ACC TGG AAT TTC TGC TCA CAG AAT TGG AGT CAG CTC CCA CTG CTG CTC Thr Trp Asn Phe Cys Ser Gln Asn Trp Ser Gln Leu Pro Leu Leu 395 400 405 410	1312
CCC AAA TTT GAT GAG GTA TAT GCC CGC TCT TAC TGC TTC TCA GCC AAC Pro Lys Phe Asp Glu Val Tyr Ala Arg Ser Tyr Cys Phe Ser Ala Asn 415 420 425	1360
TAC ATC TAC CAC TTG TTT GTG AAC GGT TAC AAA TTC ACA GAG GAG ACT Tyr Ile Tyr His Leu Phe Val Asn Gly Tyr Lys Phe Thr Glu Glu Thr 430 435 440	1408
TGG CCC CAA ATA CAC TTT GAA AAA GAA GTG GGG AAT AGC AGC ATA GCC Trp Pro Gln Ile His Phe Glu Lys Glu Val Gly Asn Ser Ser Ile Ala 445 450 455	1456
TGG TCT CTT GGC TAC ATG CTC AGC CTG ACC AAC CAG ATC CCA GCT GAA Trp Ser Leu Gly Tyr Met Leu Ser Leu Thr Asn Gln Ile Pro Ala Glu 460 465 470	1504
AGC CCT CTG ATC CGT CTG CCC ATA GAA CCA CCT GTC TTT GTG GGC ACC Ser Pro Leu Ile Arg Leu Pro Ile Glu Pro Val Phe Val Gly Thr 475 480 485 490	1552

FIG. 6 (cont'd.)

9598-066

(SHEET 12 OF 16)

CTC GCT TTC TTC ACA GTG GCA GCC TTG CTG TGT CTG GCA TTT CTT GCA	1600
Leu Ala Phe Phe Thr Val Ala Ala Leu Leu Cys Leu Ala Phe Leu Ala	
495 500 505	
TAC CTG TGT TCA GCA ACC AGA AGA AAG AGG CAC TCC GAG CAT GCC TTT	1648
Tyr Leu Cys Ser Ala Thr Arg Arg Lys Arg His Ser Glu His Ala Phe	
510 515 520	
GAC CAT GCA GTG GAT TCT GAC TGAGCCTTC AAGCAGCTCC TGGAGTCCAA TGGC	1703
Asp His Ala Val Asp Ser Asp	
525	
TGCTTAGAGT CAGCTGGGT GGCACCAGGC AATGCAGGTG AAGTGGCTGC CTTCAGGAAA	1763
TACAACTAAC TAAAATCAAAC CACCTAGTC ACGTGCTCT CAAATACTGA TTTCTGCCAC	1823
AGCACCTCTT GAGGCATCCC TTGGCTATTCT TGTGCATATT GTTCTTCAGA GACCTCACTA	1883
CCCACATGCT GATCTATTGG GGAACAGAGA AGAGACAGGC CACTAAGTC AGGCTCTTTA	1943
TATTAAGTTCC CCCAGAGGAA GAGTAAGTTG AGAAGGTATC AGTTAACATGT TGAAGAATTG	2003
ACCTCAGGGC TCAGTTTCCA TTTCCTTCCC TCAGTATTCT TCCCTGGCAAG ATACCCATTA	2063
AGCATTTCGC CAATCAGAAAT CTCACTTTAT AGTTTTTCCC ATTGGTCTTT AACTAAGACT	2123
TTCTTGTAGC AATCTCGTAA GCAGTGAACC CCCTCAGATC AGTAGAAATAT AGTATCTGGG	2183
GGAGAAGACT TACTTCCTTC AGGGCAGCAG CCACAGCCAG GCTTCTGTCA TACAGGTAGA	2243
TCCCCAGCA CAGAGACATA AAAAAGGTCT CCCAGAAAAC TATAGACCAT TCTCCAAGTG	2303
GAATTCCAC TTAGGGCTCT GGTCAGTAA TTGCAACCTG TGTTGGTTC ATCATCCTCA	2363
TCTCACCATT GTATTGCTAT GCCCTCCCAT AAAAACACAT TGATCCCTAG CAAGATTATT	2423
GCATTCCAGA TTTTACTGCC TTTCCTAGGC TTTCGCTTAG CAAAGGGCTG ACTTTCCATT	2483
GTTATCATGG TGTATATATT TTTCACCA TCCCCACAAAG TATACTTGAT GTTGTCTAG	2543
AACGAACATC CTACTCTATG ATTACTAAC CAATTACTTT CCCAGATCAT AGACCTCTCT	2603
GCATAGTAGT CATAGGTCTT GACTTTGGGG AAAGAAAAGG AAGCTGCAGG AATATTATC	2663
TCCAAAGTCG AATGAGAAAG AACTCCAGCA AATCCAATGG CTACAAACTA AAAATCAGCA	2723
TTATTTCTATA TTGCTGTTTC TTAGCTGAAT ATGGAATAAA GAACTATTAT TTTATTTGA	2783
AAAAAAAAAA AAAA	2797

F: G. 6 (cont.d)

9598-066

(SHEET 13 OF 16)

GCAGCGCGGT TTTCTTGT CCTGGTCAAC AAAGAAATGT GGAGTGTCTT GGCTGAATCC TCATACAGC AAGATCATTA TGTTGCTGTT AGGTAGGACT TGTATCCAGA TGTAAGGTTG AAAAAGTGAT ATAATAAAGG AACCAAGGAG AAAATTAGA AGGAAAGAAA AAATTGCCTC TGCAGGTGT CGAGCAGGAT TGCTTCTGCA ACAAAAGCCT CCACCCAGCC ACATCTTGGG AAAAGA ATG GCC ACT TCT TGG GGC ACA GTC TTT TTC ATG CTG GTG GTA Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val	60 120 180 240 288
1 5 10	
TCC TGT GTT TGC AGC GCT GTC TCC CAC AGG AAC CAG CAG ACT TGG TTT Ser Cys Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe 15 20 25 30	336
GAG GGT ATC TTC CTG TCT TCC ATG TGC CCC ATC AAT GTC AGC GCC AGC Glu Gly Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser 35 40 45	384
ACC TTG TAT GGA ATT ATG TTT GAT GCA GGG AGC ACT GGA ACT CGA ATT Thr Leu Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr Gly Thr Arg Ile 50 55 60	432
CAT GTT TAC ACC TTT GTG CAG AAA ATG CCA GGA CAG CTT CCA ATT CTA His Val Tyr Thr Phe Val Gln Lys Met Pro Gly Gln Leu Pro Ile Leu 65 70 75	480
GAA GGG GAA GTT TTT GAT TCT GTG AAG CCA GGA CTT TCT GCT TTT GTA Glu Gly Glu Val Phe Asp Ser Val Lys Pro Gly Leu Ser Ala Phe Val 80 85 90	528
GAT CAA CCT AAG CAG GGT GCT GAG ACC GTT CAA GGG CTC TTA GAG GTG Asp Gln Pro Lys Gln Gly Ala Glu Thr Val Gln Gly Leu Leu Glu Val 95 100 105 110	576
GCC AAA GAC TCA ATC CCC CGA AGT CAC TGG AAA AAG ACC CCA GTG GTC Ala Lys Asp Ser Ile Pro Arg Ser His Trp Lys Lys Thr Pro Val Val 115 120 125	624
CTA AAG GCA ACA GCA GGA CTA CGC TTA CTG CCA GAA CAC AAA GCC AAG Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Glu His Lys Ala Lys 130 135 140	672
GCT CTG CTC TTT GAG GTA AAG GAG ATC TTC AGG AAG TCA CCT TTC CTG Ala Leu Leu Phe Glu Val Lys Glu Ile Phe Arg Lys Ser Pro Phe Leu 145 150 155	720
GTA CCA AAG GGC AGT GTT AGC ATC ATG GAT GGA TCC GAC GAA GGC ATA Val Pro Lys Gly Ser Val Ser Ile Met Asp Gly Ser Asp Glu Gly Ile 160 165 170	768
TTA GCT TGG GTT ACT GTG AAT TTT CTG ACA GGT CAG CTG CAT GGC CAC Leu Ala Trp Val Thr Val Asn Phe Leu Thr Gly Gln Leu His Gly His 175 180 185 190	816
AGA CAG GAG ACT GTG GGG ACC TTG GAC CTA GGG GGA GCC TCC ACC CAA Arg Gln Glu Thr Val Gly Thr Leu Asp Leu Gly Gly Ala Ser Thr Gln 195 200 205	864
ATC ACG TTC CTG CCC CAG TTT GAG AAA ACT CTG GAA CAA ACT CCT AGG Ile Thr Phe Leu Pro Gln Phe Glu Lys Thr Leu Glu Gln Thr Pro Arg 210 215 220	912
GGC TAC CTC ACT TCC TTT GAG ATG TTT AAC AGC ACT TAT AAG CTC TAT Gly Tyr Leu Thr Ser Phe Glu Met Phe Asn Ser Thr Tyr Lys Leu Tyr 225 230 235	960

FIG. 7

9598-066

"SHEET 14 OF 16)

ACA CAT AGT TAC TTG GGA TTT GGA TTG AAA GCT GCA AGA CTA GCA ACC Thr His Ser Tyr Leu Gly Phe Gly Leu Lys Ala Ala Arg Leu Ala Thr 240 245 250	1008
CTG GGA GCC CTG GAG ACA GAA GGG ACT GAT GGG CAC ACT TTC CGG AGT Leu Gly Ala Leu Glu Thr Glu Gly Thr Asp Gly His Thr Phe Arg Ser 255 260 265 270	1056
GCC TGT TTA CCG AGA TGG TTG GAA GCA GAG TGG ATC TTT GGG GGT GTG Ala Cys Leu Pro Arg Trp Leu Glu Ala Glu Trp Ile Phe Gly Gly Val 275 280 285	1104
AAA TAC CAG TAT GGT GGC AAC CAA GAA GGG GAG GTG GGC TTT GAG CCC Lys Tyr Gln Tyr Gly Gly Asn Gln Glu Gly Glu Val Gly Phe Glu Pro 290 295 300	1152
TGC TAT GCC GAA GTG CTG AGG GTG GTA CGA GGA AAA CTT CAC CAG CCA Cys Tyr Ala Glu Val Leu Arg Val Val Arg Gly Lys Leu His Gln Pro 305 310 315	1200
GAG GAG GTC CAG AGA GGT TCC TTC TAT GCT TTC TCT TAC TAT TAT GAC Glu Glu Val Gln Arg Gly Ser Phe Tyr Ala Phe Ser Tyr Tyr Tyr Asp 320 325 330	1248
CGA GCT GTT GAC ACA GAC ATG ATT GAT TAT GAA AAG GGG GGT ATT TTA Arg Ala Val Asp Thr Asp Met Ile Asp Tyr Glu Lys Gly Gly Ile Leu 335 340 345 350	1296
AAA GTT GAA GAT TTT GAA AGA AAA GCC AGG GAA GTG TGT GAT AAC TTG Lys Val Glu Asp Phe Glu Arg Lys Ala Arg Glu Val Cys Asp Asn Leu 355 360 365	1344
GAA AAC TTC ACC TCA GGC AGT CCT TTC CTG TGC ATG GAT CTC AGC TAC Glu Asn Phe Thr Ser Gly Ser Pro Phe Leu Cys Met Asp Leu Ser Tyr 370 375 380	1392
ATC ACA GCC CTG TTA AAG GAT GGC TTT GGC TTT GCA GAC AGC ACA GTC Ile Thr Ala Leu Leu Lys Asp Gly Phe Gly Ala Asp Ser Thr Val 385 390 395	1440
TTA CAG CTC ACA AAG AAA GTG AAC AAC ATA GAG ACG GGC TGG GCC TTG Leu Gln Leu Thr Lys Lys Val Asn Asn Ile Glu Thr Gly Trp Ala Leu 400 405 410	1488
GGG GCC ACC TTT CAC CTG TTG CAG TCT CTG GGC ATC TCC CAT TGAGGCCAC Gly Ala Thr Phe His Leu Leu Gln Ser Leu Gly Ile Ser His 415 420 425	1539
GTACTTCCCTT GGAGACCTGC ATTTGCCAAC ACCTTTTAA GGGGAGGAGA GAGCACTTAG TTCTGAACT AGTCTGGAC ATCTGGAAC TGAGCTAGA GATTTAGGT TAATTAAATT TACACATCTA ATGTGAAC TGCTGCTAACCTCAACCTCAACTGACCTCAAGAGT ACACAGCTGG CACCAGAGCA TCACAGAGAG CCCTGTGAGC CAAAAAGTAT AGTTTGAA CTTAACCTTG GAGTGAGAGC CCAGGGACAG GTCCCTGGAA ACCAAAGAAA AATCGCATTT CAACCCCTTG AGTGCCTCAT TCCACTGAAT ATTTAAATT TCCTCTTAAA TGGTAAACTG ACTTATTGCA ATCCCAAGAC CCATCAATAT CAGTATTTT TTCCCTCCCTA TACAGTGCCTC TGCCCCACCT TATCTGCACC CACCTCCCT GAAAAAGAGA GAAAAAAA AAAAAAAA	1599 1659 1719 1779 1839 1899 1959 1998

Fig. 7 (cont'd.)

9598-066

HEET 15 OF 16)

CD39L2 1 MKKGIRYETSRKTSYIFQQPQHGPWMQTRXRKISNHGSLRVAKVATPLGICVGVFVTVW
 CD39L4 1 -
 CD39L1 1 -
 CD39L3 1 -
 CD39 1 -

ACR 1

ACR II

CD39L2 120 FT-KPPR-TPT-HEAFK VN PG-SAYAD-V N JAO-CRELL-VAKODIP-PDFW-NVPL
 CD39L4 67 VQXKQNPOLPQHGEEDSVK DG-SALVDPNTR-AVQDLEVKDPSRSHTKIPF
 CD39L1 58 NPA-KENDTGTGIVCGH-ECDVEGCGIS-HADPHGKTHOS-VGCCLPDNLQDPRSHKETPL
 CD39L3 75 SPAEELMINTGWHOTPCVSXKGAGIS-WHMP-IVPRP-PECGCNAVKGQPSHLQCTPL
 CD39 67 SPAEELMINTGWHOTPCVSXKGAGIS-WHMP-IVPRP-PECGCNAVKGQPSHLQCTPL

ACB II

CD39L2	178	VLLATAGCRLLL...PEKERA...LLEVKKEFPRSPFLVGGDCVSVINCGTFCVSLWITNN
CD39L4	126	VLLATAGCRLLL...PEKAKAKA...LLEVKKEFPRSPFLVPGKCVSIVNCGTCFCVSLWITNN
CD39L1	118	YLGATAGCHRLRLL...LTPKEAATTSVLMVTEVLTQTYPF...DFRGARLIGQEECVLYGWNTINY
CD39L3	135	YLGATAGCHRLRLL...LTPKEAATTSVLMVTEVLTQTYPF...DFRGARLIGQEECVLYGWNTINY
CD39	127	YLGATAGCHRLRLN...SELALATVILVUVKRSLSNPF...DFRGARLIGQEECVLYGWNTINY

ACR III

ACR IV

CD39L2	235	WTGSSL	WPGSGEAVGMLDLSGG_	STOIAFLPRVETTLASPPGTYLTALR
CD39L4	183	WTGSSL	WGHROETVGLDLSGCASTOITFPLPEKTLQTPGTYLTSTY	
CD39L1	176	WGLNEPDKYGNVGRGP . . .	WGLNEPDKYGNVGRGP . . . P1_KOTHTGA_DLGGAACSTOITFETTSPEDRASE . . . P1_PLB	
CD39L3	193	WPGSGEAVGMLDLSGG_	WPGSGEAVGMLDLSGG_	
CD39	185	WGLNEPDKTPEAVGMLDLSGG_	WGLNEPDKTPEAVGMLDLSGG_	

CD39L2	283	M-N-E-T-Y-K-L-Y-I-M-S-D-G-L-G-L-M-S-A-R-L-A-L-G-C-H-E-C-O-P-R-I-C-G-L-E-L-V-E-P-C-L-G-F-S-F-K-E-S-W-I-H-E-V-T-Y-R
CD39L4	231	A-N-G-T-V-E-L-Y-T-H-S-L-G-C-H-L-A-R-L-A-L-G-A-E-T-1-E-N-D-G-H-T-F-R-S-A-C-L-P-F-M-L-E-H-E-T-F-C-G-V-E-Y-R
CD39L1	229	Y-Q-C-G-E-M-Y-V-T-H-S-F-L-C-Y-G-H-D-Q-V-L-Q-P-D-L-E-B-A-L-O-1-E-N-T-H-C-P-C-M-G-F-S-V-L-E-C-G-V-Y-O-S
CD39L3	246	Y-G-V-E-T-L-Y-T-H-S-F-Q-C-Y-G-H-T-E-A-K-K-F-L-E-A-L-L-O-M-E-T-K-H-N-H-P-C-M-P-D-B-S-I-S-T-C-H-G-V-E-S

CD39L2 485
CD39L4 429
CD39L1 432 ERKGTFSIEMVLLLEGRALIATWHLTFRQVHNLSEPLTI*
CD39L3 478 ERLTEPVEPVGDTAFFLNLCLPAPLTCISRERKRSHEAFDHAVIDSD*
CD39 468 DSTDPMHSLEEVLPVPGFSLIVLVEVARQGMLFHKPSYEWMDW*

F, G, &

ACR

peaGDP	2 EELKLITFHSFSPLIHSQYLGNNM. LTSRKIFVVEBISYYAH. FDAGSTGSR H VY
potapyrase	6 SREHFLPFLVFLPLLSLSSLNVNAOI. DPERRLHSHSE. .LYAHFDAGSTGSRVHVY
CD39L2	61 KHEERATQAFFS. TRVPGAREQD. B. SPLN. IAI. GHEVTV. LHDAGSTGSRVHVY
CD39L4	7 TAEF. DAVVFCVC. CAV. FHRNGC. THFEGH. .LSS. CF. HV. SASTLY. LHDAGSTGSRVHVY
dNTase	37 KISFLCL. IIISVLL. LLFVFGV. FSEN. A. SP. PLR. SKFQ. SKV. VO. YAH. LHDAGSTGSRVHVY
yGDPase	5 D. G. H. I. N. D. E. P. G. Y. Q. L. D. S. C. Y. O. P. E. L. A. D. K. S. Q. N. S. Q. T. C. S. E. H. .Y. V. I. H. L. D. A. G. S. T. G. S. R. V. H. Y.

ACR II

paaGDP 61 EPNQNLDDLEIISKG EYR R WPGLSSYA PEQAAASLIPLL QRE D V P E D D L Q K T P V
 potapyrase 63 F E P K L G L L P C I M N E Y P T P E W P G L S S A D P K I A A S L I P L L D C G V V P O P L O S E T P V
 CD39L2 119 QFT I E P R E T P I T T H E T P K A V P G L S S Y A D D V E K I A T C R E L L D V A R Q D P C P C F R A T P V
 CD39L4 66 T P V Q N P P G Q L D I L E G E V F D V K P G L S S V D Q P R Q P A E I C L L V A R D S P S R H K T P V
 dNTPase 96 K F I R R S F I D H N L L Y K E F P K P G L S S A P P A A E S K L L D E A A F P M E S S T P V
 yGDPase 65 K F P I I C T S P T I L D E K F D I E P K P G L S S D T D S V C A A S L I P L L V A N V A V P V I P C T P V

ACR II

peaGDP	121	RG-CATAGLRLNGDA-EKILQ-SVRD-LSN-PSTF-NV-S-PAVSI-DCT-OEGGYL-WVTVNFA
potapyrase	123	MUG-CATAGLRLNGDA-EKILQ-SVRD-LSN-PSTF-XSDGQWV-NI-DGT-EGEPMH-NYL
CD39L2	178	YVKATAGLRLPGR-KAK-A-LQKV-V-FF-ASPIR-EVGDC-VSIS-MC-DEG-V-EAW-TVNL
CD39L4	126	YVKATAGLRLPGR-KAK-A-LQKV-V-FF-ASPIR-EVGDC-VSIS-MC-DEG-V-EAW-TVNL
dNTTPase	156	YVKATAGLRLPGR-SKAHL-A-SVRLDFA-KSES-SV-MDA-VEIN-LIGT-DEG-E-V-TVNL
vGDPase	123	A-KATAGLRLGDA-EKILQ-SVRD-LSN-PSTF-XDGP-EVGDC-VSIS-MC-DEG-EV-TVNL

ACR III

ACR IV

peaGDP	180	LGNLKGK ^{WTX}	.TIVGVLDLGGGSVYHAAAVSKXTARNAPKVADGDPYKIVVVLKGIPYR
potapyrase	182	HGLHLGRGMS	.PEVLDLGGGSVYHAAAVSLPQGFAKANPQEDGSPYCRHRLKGDYN
CD19L2	236	TGSLKTPGGS	.IYGVLDDLGGSSTCIAFLPRVEG.....TKEASPPFGYLTAERDFNTYK
CD19L4	184	TGSLKTPGGS	.TIVGVLDLGGGSVYHAAAVSKXTARNAPKVADGDPYKIVVVLKGIPYR
DNPase	214	EGRLSLTGMQH	.LEGLGGGSVYHAAAVSKXTARNAPKVADGDPYKIVVVLKGIPYR

ACB IV

peaGDP	238	LYVHSYLEFGRLAAGRABILNLNLTPESE.	MPCLLAAGFNG.	YY
potapyrase	239	LYVHSYLEFGQLAACTAEIFKRSNES.	MPCALECFCG.	YY
CD39L2	289	LYTHSYLGLCGLKAABRATLGLCTECPKKGDRGV.	SPCLSPBPKG.	BN
CD39L4	237	LYTHSYLGLCGLKAABRATLGLCTECPKKGDRGV.	SACLPRVLE.	BL
INTPase	264	WETHSYLGLCGLKAABRATLGLCTECPKKGDRGV.	SYCNMPILAH.	RDN
intPase	229	LYVHSYLEFGQLAACTAEIFKRSNES.	SPCLSPBPKG.	BN

ootapyrase	452	AS+
IDS9L2	483	AS-
IDS9L4	429	---
INTPase	462	---
cGDPase	471	OS+

Fig. 9